

Exhibit I

Query: SEQ ID NO: 7

BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit](#) [and Resubmit](#) [Save](#) [Search Strategies](#) [Formatting options](#) [Download](#)

Nucleotide Sequence (17 letters)

Results for: Icl|11866 None(17bp) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
Icl|11866

Description
None

Molecule type
nucleic acid

Query Length
17

Database Name
nr

Description
All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)

Program
BLASTN 2.2.19+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Database

Posted date	Dec 28, 2008 5:47 PM
Number of letters	252,991,180
Number of sequences	7,851,115
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

Results Statistics

Length adjustment	15
Effective length of query	2
Effective length of database	25605224455
Effective search space	51210448910
Effective search space used	51210448910

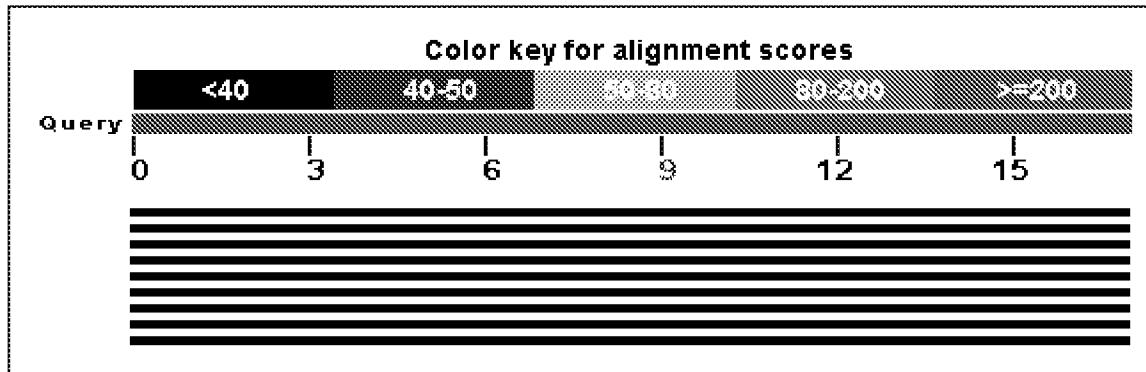
Designing or Testing PCR Primers? Try your s

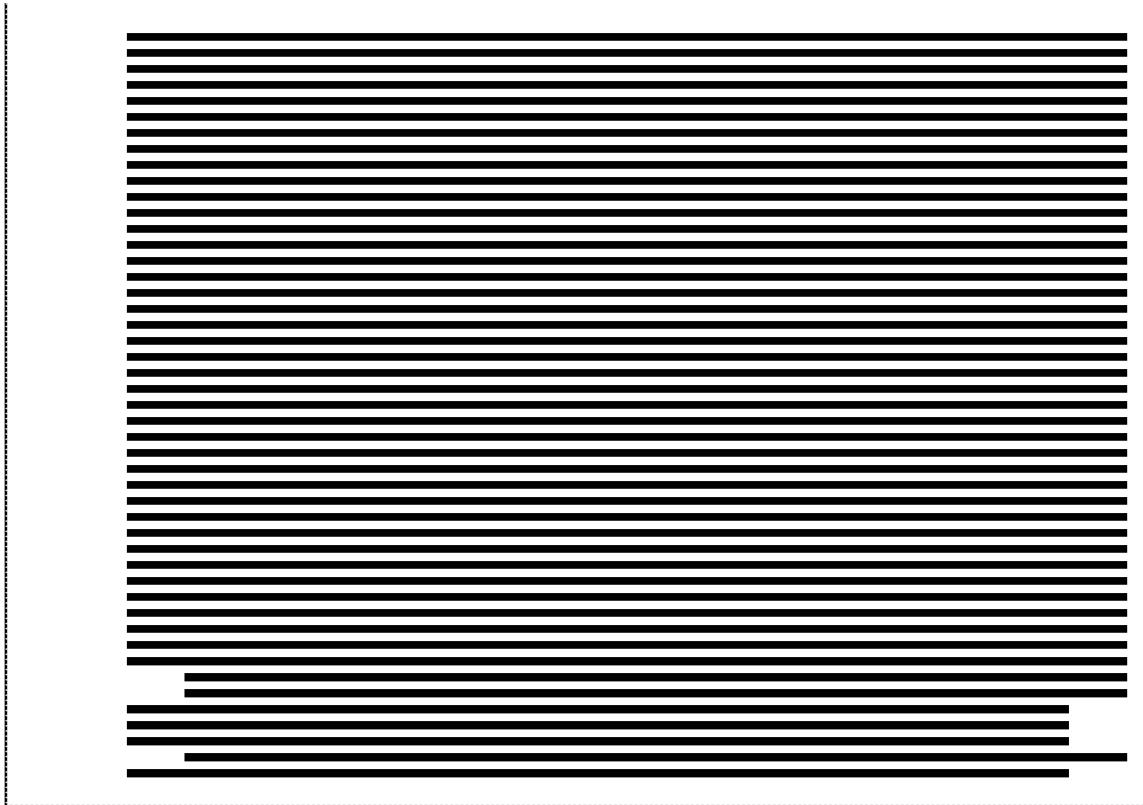
Graphic Summary

Distribution of 129 Blast Hits on the Query Sequence

?

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:
(Click headers to sort columns)

NW_002196569.1	Ralstonia solanacearum IPO1609 >emb CU914168.1 Ralstonia solanacearum strain IPO1609 Genome Draft	34.2 34.2 100% 2.6 100%
NW_002196522.1	Ralstonia solanacearum MolK2 >emb CU694390.1 Ralstonia solanacearum strain MolK2 Genome Draft	34.2 34.2 100% 2.6 100%
XM_001915641.1	PREDICTED: Equus caballus similar to Glutathione peroxidase 2 (GSHPx-2) (GPx-2) (Glutathione peroxidase- gastrointestinal) (GSHPx-GI) (LOC100146145), mRNA	34.2 34.2 100% 2.6 100% 
XM_001916096.1	PREDICTED: Equus caballus similar to glutathione peroxidase 1 (LOC100053396), mRNA	34.2 34.2 100% 2.6 100% 
CP000958.1	Burkholderia cenocepacia MC0-3 chromosome 1, complete sequence	34.2 112 100% 2.6 100%
NM_001115119.1	Canis lupus familiaris glutathione peroxidase 1 (GPX1), mRNA	34.2 34.2 100% 2.6 100% 
XR_038530.1	PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA	34.2 34.2 100% 2.6 100% 
XR_038228.1	PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA	34.2 34.2 100% 2.6 100% 
NM_001077512.2	Pan troglodytes glutathione peroxidase 1 (GPX1), mRNA	34.2 34.2 100% 2.6 100% 
CP000458.1	Burkholderia cenocepacia HI2424 chromosome 1, complete sequence	34.2 112 100% 2.6 100%
AK239914.1	Sus scrofa mRNA, clone:UTR010010G07, expressed in uterus	34.2 34.2 100% 2.6 100% 
AK231261.1	Sus scrofa mRNA, clone:ITT010025D10, expressed in intestine	34.2 34.2 100% 2.6 100% 
AB121000.1	Callithrix jacchus gpxl mRNA for glutathione peroxidase 1, complete cds	34.2 34.2 100% 2.6 100%
AB120996.1	Pan troglodytes gpxl mRNA for glutathione peroxidase 1, complete cds	34.2 34.2 100% 2.6 100% 
CT573213.2	Frankia alni str. ACN14A chromosome, complete sequence	34.2 86.7 100% 2.6 100%
AK225835.1	Homo sapiens mRNA for Glutathione peroxidase 1 variant, clone: FCC127C01	34.2 34.2 100% 2.6 100% 
XR_013650.1	PREDICTED: Macaca mulatta similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) (LOC706732), mRNA	34.2 34.2 100% 2.6 100% 
CP000380.1	Burkholderia cenocepacia AU 1054 chromosome 3, complete sequence	34.2 34.2 100% 2.6 100%
AY966403.1	Callithrix jacchus cytosolic glutathione peroxidase (Gpx-1) mRNA, complete cds	34.2 34.2 100% 2.6 100%
CP000151.1	Burkholderia sp. 383 chromosome 1, complete sequence	34.2 60.5 100% 2.6 100%
BC007865.2	Homo sapiens glutathione peroxidase 1,	34.2 34.2 100% 2.6 100% 

mRNA (cDNA clone MGC:14399 IMAGE:4301275), complete cds									
BC000742.2	Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:2335 IMAGE:3505654), complete cds	34.2	34.2	100%	2.6	100%			
BC070258.1	Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:88245 IMAGE:6452792), complete cds	34.2	34.2	100%	2.6	100%			
AY572225.1	Canis familiaris glutathione peroxidase 1 mRNA, partial cds	34.2	34.2	100%	2.6	100%			
AC135371.2	Homo sapiens X BAC RP11-142G7 (Roswell Park Cancer Institute Human BAC Library) complete sequence	34.2	34.2	100%	2.6	100%			
AY327818.1	Homo sapiens glutathione peroxidase 1 (GPX1) gene, complete cds	34.2	34.2	100%	2.6	100%			
NM_214201.1	Sus scrofa glutathione peroxidase 1 (GPX1), mRNA >gb AF532927.1 Sus scrofa cytosolic glutathione peroxidase (GPX1) mRNA, complete cds	34.2	34.2	100%	2.6	100%			
AB120999.1	Cebus apella gpx1 mRNA for glutathione peroxidase 1, complete cds	34.2	34.2	100%	2.6	100%			
AB120998.1	Hylobates lar gpx1 mRNA for glutathione peroxidase 1, complete cds	34.2	34.2	100%	2.6	100%			
AB120997.1	Pongo pygmaeus gpx1 mRNA for glutathione peroxidase 1, complete cds	34.2	34.2	100%	2.6	100%			
DQ333996.1	Spermophilus parryii clone SP00035 glutathione peroxidase 1 mRNA, partial cds	34.2	34.2	100%	2.6	100%			
M83094.1	Homo sapiens cytosolic selenium-dependent glutathione peroxidase gene, complete cds, and rhoh12 gene, 3' end	34.2	34.2	100%	2.6	100%			
Y00483.1	Human gene for glutathione peroxidase	34.2	34.2	100%	2.6	100%			
Y00433.1	Human mRNA for glutathione peroxidase (EC 1.11.1.9.)	34.2	34.2	100%	2.6	100%			
X13710.1	H.sapiens unspliced mRNA for glutathione peroxidase	34.2	34.2	100%	2.6	100%			
X13709.1	Human gpx1 mRNA for glutathione peroxidase	34.2	34.2	100%	2.6	100%			
NM_001085444.1	Oryctolagus cuniculus glutathione peroxidase 1 (GPX1), mRNA >emb X13837.1 OCGPO Rabbit mRNA for glutathione peroxidase (EC 1.11.1.9.)	34.2	34.2	100%	2.6	100%			
M21304.1	Human glutathione peroxidase (GPX1) mRNA, complete cds	34.2	34.2	100%	2.6	100%			
U39842.1	Cavia porcellus glutathione peroxidase mRNA, partial cds	34.2	34.2	100%	2.6	100%			
CR626479.1	full-length cDNA clone CS0CAP001YI17 of Thymus of Homo sapiens (human)	34.2	34.2	100%	2.6	100%			
CR620255.1	full-length cDNA clone CS0DD004YA07 of Neuroblastoma Cot 50-normalized of Homo sapiens (human)	34.2	34.2	100%	2.6	100%			
CR614747.1	full-length cDNA clone CS0DI086YP09 of Placenta Cot 25-normalized of Homo sapiens (human)	34.2	34.2	100%	2.6	100%			
CR601795.1	full-length cDNA clone CS0DI068YJ17 of	34.2	34.2	100%	2.6	100%			

	Placenta Cot 25-normalized of Homo sapiens (human)														
CR595371.1	full-length cDNA clone CS0DC025YE23 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	34.2	34.2	100%	2.6	100%									
AK130160.1	Homo sapiens cDNA FLJ26650 fis, clone MPE04848, highly similar to Glutathione peroxidase (EC 1.11.1.9)	34.2	34.2	100%	2.6	100%									
AC121247.2	Homo sapiens chromosome 3 clone RP11-3B7, complete sequence	34.2	34.2	100%	2.6	100%									
AB105162.1	Macaca fuscata mRNA for cytosolic glutathione peroxidase, complete cds	34.2	34.2	100%	2.6	100%									
NM_000581.2	Homo sapiens glutathione peroxidase 1 (GPX1), transcript variant 1, mRNA	34.2	34.2	100%	2.6	100%									
NM_201397.1	Homo sapiens glutathione peroxidase 1 (GPX1), transcript variant 2, mRNA	34.2	34.2	100%	2.6	100%									
CP001111.1	Stenotrophomonas maltophilia R551-3, complete genome	32.2	32.2	94%	10	100%									
AB098194.1	Codonosiga gracilis CgPTK-f mRNA for receptor-type protein tyrosine kinase, complete cds	32.2	32.2	94%	10	100%									
CP000058.1	Pseudomonas syringae pv. phaseolicola 1448A, complete genome	32.2	32.2	94%	10	100%									
AF396866.1	Bacteriophage Mx8, complete genome	32.2	32.2	94%	10	100%									
BX950851.1	Erwinia carotovora subsp. atroseptica SCRI1043, complete genome	32.2	32.2	94%	10	100%									
AY596297.1	Haloarcula marismortui ATCC 43049 chromosome I, complete sequence	32.2	84.7	94%	10	100%									
AE015451.1	Pseudomonas putida KT2440 complete genome	32.2	32.2	94%	10	100%									
J05222.1	Halobacterium marismortui ribosomal protein gene cluster	32.2	32.2	94%	10	100%									
CP001322.1	Desulfatibacillum alkenivorans AK-01, complete genome	30.2	30.2	88%	41	100%									
AM920436.1	Penicillium chrysogenum Wisconsin 54-1255 complete genome, contig Pc00c21	30.2	84.7	94%	41	100%									
AC232899.1	Oryza officinalis clone OO_Ba0111F15, complete sequence	30.2	30.2	88%	41	100%									
AM747721.1	Burkholderia cenocepacia J2315 chromosome 2, complete genome	30.2	56.5	94%	41	100%									
CP000854.1	Mycobacterium marinum M, complete genome	30.2	56.5	88%	41	100%									
CP001026.1	Burkholderia ambifaria MC40-6 chromosome 2, complete sequence	30.2	56.5	100%	41	100%									
NW_001914855.1	Podospora anserina DSM 980 genomic scaffold chrm1_SC2 >emb CU633901.1 Podospora anserina genomic DNA chromosome 1, supercontig 2	30.2	30.2	88%	41	100%									
CP000959.1	Burkholderia cenocepacia MC0-3 chromosome 2, complete sequence	30.2	30.2	88%	41	100%									
XR_017747.2	PREDICTED: Homo sapiens misc_RNA (LCN1L1), miscRNA	30.2	30.2	88%	41	100%									
EU137666.1	Myxococcus fulvus strain 124B02 plasmid pMF1, complete sequence	30.2	30.2	88%	41	100%									

Designing or Testing PCR Primers? Try your sequence in the NCBI BLAST search engine.

Alignments Select All Get selected sequences Distance tree of results

>ref|NW_002196569.1| Ralstonia solanacearum IPO1609
emb|CU914168.1| Ralstonia solanacearum strain IPO1609 Genome Draft
Length=3372855

Features in this part of subject sequence:
glutathione peroxidase protein

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 2635709 CTCGGCTTCCCGTGCAA 2635693

>ref|NW_002196522.1| Ralstonia solanacearum MolK2
emb|CU694390.1| Ralstonia solanacearum strain MolK2 Genome Draft
Length=237010

Features in this part of subject sequence:
glutathione peroxidase protein

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 131900 CTCGGCTTCCCGTGCAA 131916

>ref|XM_001915641.1| PREDICTED: Equus caballus similar to Glutathione peroxidase 2 (GSHPx-2) (GPx-2) (Glutathione peroxidase-gastrointestinal) (GSHPx-GI) (LOC100146145), mRNA
Length=573

GENE ID: 100146145 LOC100146145 | similar to Glutathione peroxidase 2 (GSHPx-2) (GPx-2) (Glutathione peroxidase-gastrointestinal) (GSHPx-GI) [Equus caballus]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 190 CTCGGCTTCCCGTGCAA 206

>ref|XM_001916096.1| PREDICTED: Equus caballus similar to glutathione peroxidase 2 (GSHPx-2) (GPx-2) (Glutathione peroxidase-gastrointestinal) (GSHPx-GI) (LOC100053396), mRNA

Length=606

GENE ID: 100053396 LOC100053396 | similar to glutathione peroxidase 1
[Equus caballus]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query	1	CTCGGCTTCCCCTGCAA	17
Sbjct	214	CTCGGCTTCCCCTGCAA	230

>gb|CP000958.1| Burkholderia cenocepacia MC0-3 chromosome 1, complete sequence
Length=3532883

Sort alignments for this
E value Score Percen
Query start position

Features in this part of subject sequence:
Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query	1	CTCGGCTTCCCGTGCAA	17
Sbjct	2284247	CTCGGCTTCCCGTGCAA	2284231

Features in this part of subject sequence:
short-chain dehydrogenase/reductase SDR

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query	3	CGGCTTCCCGTGC	15
Sbjct	2569429	CGGCTTCCCGTGC	2569417

Features in this part of subject sequence:
 conserved hypothetical protein

Score = 26.3 bits (13), Expect = 636
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query	1	CTCGGGCTTCCCGTGCAA	17
Sbjct	2872181	CTCGGGCTTCGCGTGCAA	2872165

Features in this part of subject sequence:
diguanylate cyclase

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query	3	CGGGCTTCCCGTGC	15
Sbjct	3526443	CGGGCTTCCCGTGC	3526455

>ref|NM_001115119.1|  Canis lupus familiaris glutathione peroxidase 1 (GPX1)
Length=838

GENE ID: 442961 GPX1 | glutathione peroxidase 1 [Canis lupus familiaris]

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||||||||||||||
 Sbjct 235 CTCGGCTTCCCGTGCAA 251

>ref|XR_038530.1|  PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA Length=876

GENE ID: 441481 LOC441481 | similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) [Homo sapiens]

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||||||||||||||
 Sbjct 253 CTCGGCTTCCCGTGCAA 269

>ref|XR_038228.1|  PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA Length=878

GENE ID: 441481 LOC441481 | similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) [Homo sapiens]

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||||||||||||||
 Sbjct 255 CTCGGCTTCCCGTGCAA 271

>ref|NM_001077512.2|  Pan troglodytes glutathione peroxidase 1 (GPX1), mRNA Length=613

GENE ID: 461015 GPX1 | glutathione peroxidase 1 [Pan troglodytes] (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||||||||||||||
 Sbjct 221 CTCGGCTTCCCGTGCAA 237

>gb|CP000458.1|  Burkholderia cenocepacia HI2424 chromosome 1, complete sequenc Length=3483902

Sort alignments for this
 E value Score Percent
 Query start position

Features in this part of subject sequence:
 Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||||||||||||||
 Sbjct 2258895 CTCGGCTTCCCGTGCAA 2258879

Features in this part of subject sequence:
short-chain dehydrogenase/reductase SDR

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query 3 CGGCTTCCCGTGC 15
|||||||||||||||
Sbjct 2528844 CGGCTTCCCGTGC 2528832

Features in this part of subject sequence:
conserved hypothetical protein

Score = 26.3 bits (13), Expect = 636
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 CTCGGCTTCCCGTGC 17
||||||||| |||||||||
Sbjct 2825631 CTCGGCTTCCCGTGC 2825615

Features in this part of subject sequence:
conserved hypothetical protein

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query 1 CTCGGCTTCCCGT 13
|||||||||||||||
Sbjct 3438094 CTCGGCTTCCCGT 3438082

>dbj|AK239914.1|  Sus scrofa mRNA, clone:UTR010010G07, expressed in uterus
Length=912

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGC 17
||||||||| |||||||||
Sbjct 312 CTCGGCTTCCCGTGC 328

>dbj|AK231261.1|  Sus scrofa mRNA, clone:ITT010025D10, expressed in intestine
Length=936

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGC 17
||||||||| |||||||||
Sbjct 327 CTCGGCTTCCCGTGC 343

>dbj|AB121000.1| Callithrix jacchus gpx1 mRNA for glutathione peroxidase 1, comp
cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGC 17
||||||||| |||||||||
Sbjct 214 CTCGGCTTCCCGTGC 230

>dbj|AB120996.1|  Pan troglodytes gpx1 mRNA for glutathione peroxidase 1, compl
cds
Length=606

GENE ID: 461015 GPX1 | glutathione peroxidase 1 [Pan troglodytes]
(10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||
Sbjct 214 CTCGGCTTCCCGTGCAA 230

>emb|CT573213.2|  Frankia alni str. ACN14A chromosome, complete sequence
Length=7497934

Sort alignments for this		
E value	Score	Percen
Query start position		

Features in this part of subject sequence:
Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||
Sbjct 1918274 CTCGGCTTCCCGTGCAA 1918290

Features flanking this part of subject sequence:
93 bp at 5' side: Putative MarR-family transcriptional regulator
53 bp at 3' side: Putative transcriptional regulator

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 4 GGCTTCCCGTGCA 16
|||||||||||||
Sbjct 641315 GGCTTCCCGTGCA 641327

Features in this part of subject sequence:
hypothetical protein; putative Amidohydrolase domain

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 3 CGGCTTCCCGTGC 15
|||||||||||||
Sbjct 1575841 CGGCTTCCCGTGC 1575853

>dbj|AK225835.1|  Homo sapiens mRNA for Glutathione peroxidase 1 variant, clo
FCC127C01
Length=874

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||

Sbjct 223 CTCGGCTTCCCGTGC 239

>ref|XR_013650.1|  PREDICTED: *Macaca mulatta* similar to Glutathione peroxidase (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) (LOC706732), mRNA Length=811

GENE ID: 706732 LOC706732 | similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) [Macaca mulatta]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query	1	CTCGGCTTCCCGTGC _{AA}	17
Sbjct	205	CTCGGCTTCCCGTGC _{AA}	221

>gb|CP000380.1| Burkholderia cenocepacia AU 1054 chromosome 3, complete sequen
Length=1196094

Features in this part of subject sequence:
Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query	1	CTCGGGCTTCCCGTGC	17
Subj	632809	CTCGGGCTTCCCGTGC	632825

>gb|AY966403.1| Callithrix jacchus cytosolic glutathione peroxidase (Gpx-1) mRNA
complete cds
Length=858

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query	1	CTCGGCTTCCGTGCAA	17
Sbjct	237	CTCGGCTTCCGTGCAA	253

>gb|CP000151.1| Burkholderia sp. 383 chromosome 1, complete sequence
Length=3694126

Sort alignments for this
E value Score Percen
Query start position

Features in this part of subject sequence:
Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query	1	CTCGGCTTCCCGTGC ^{AA}	17
Sbjct	2403347	CTCGGCTTCCCGTGC ^{AA}	2403331

Features in this part of subject sequence:
 conserved hypothetical protein

Score = 26.3 bits (13), Expect = 636
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Minus

```
Query 1      CTCGGCTTCCCGTGCAA  17
          ||||||| ||||| ||||| |
Sbjct 3002445 CTCGGCTTCCCGTGCAA  3002429
```

>gb|BC007865.2|  Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC: IMAGE:4301275), complete cds
Length=851

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA  17
          ||||||| ||||| ||||| ||||| |
Sbjct 230    CTCGGCTTCCCGTGCAA  246
```

>gb|BC000742.2|   Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MG IMAGE:3505654), complete cds
Length=863

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA  17
          ||||||| ||||| ||||| ||||| |
Sbjct 243    CTCGGCTTCCCGTGCAA  259
```

>gb|BC070258.1|   Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MG IMAGE:6452792), complete cds
Length=866

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA  17
          ||||||| ||||| ||||| ||||| |
Sbjct 236    CTCGGCTTCCCGTGCAA  252
```

>gb|AY572225.1|  Canis familiaris glutathione peroxidase 1 mRNA, partial cds
Length=434

GENE ID: 442961 GPX1 | glutathione peroxidase 1 [Canis lupus familiaris]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA  17
          ||||||| ||||| ||||| ||||| |
Sbjct 175    CTCGGCTTCCCGTGCAA  191
```

>gb|AC135371.2|  Homo sapiens X BAC RP11-142G7 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Length=25901

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 8993 CTCGGCTTCCCGTGCAA 8977

>gb|AY327818.1|  Homo sapiens glutathione peroxidase 1 (GPX1) gene, complete cds
Length=4877

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 2385 CTCGGCTTCCCGTGCAA 2401

>ref|NM_214201.1|  Sus scrofa glutathione peroxidase 1 (GPX1), mRNA
gb|AF532927.1|  Sus scrofa cytosolic glutathione peroxidase (GPX1) mRNA, complete cds
Length=803

GENE ID: 397403 GPX1 | glutathione peroxidase 1 [Sus scrofa]
(10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 235 CTCGGCTTCCCGTGCAA 251

>dbj|AB120999.1| Cebus apella gpx1 mRNA for glutathione peroxidase 1, complete cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 214 CTCGGCTTCCCGTGCAA 230

>dbj|AB120998.1| Hylobates lar gpx1 mRNA for glutathione peroxidase 1, complete cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 214 CTCGGCTTCCCGTGCAA 230

>dbj|AB120997.1| Pongo pygmaeus gpx1 mRNA for glutathione peroxidase 1, complete cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)

Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||||||||||||||||
 Sbjct 214 CTCGGCTTCCCGTGCAA 230

>gb|DQ333996.1| Spermophilus parryii clone SP00035 glutathione peroxidase 1 mRNA
 partial cds
 Length=210

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||||||||||||||||
 Sbjct 65 CTCGGCTTCCCGTGCAA 81

>gb|M83094.1|HUMGLPEX  Homo sapiens cytosolic selenium-dependent glutathione gene, complete cds, and rhoh12 gene, 3' end
 Length=4407

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||||||||||||||||
 Sbjct 2774 CTCGGCTTCCCGTGCAA 2790

>emb|Y00483.1|HSGSHPX  Human gene for glutathione peroxidase
 Length=1733

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
 (Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||||||||||||||||
 Sbjct 687 CTCGGCTTCCCGTGCAA 703

>emb|Y00433.1|HSGSHPX  Human mRNA for glutathione peroxidase (EC 1.11.1.9.)
 Length=1134

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
 (Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||||||||||||||||
 Sbjct 532 CTCGGCTTCCCGTGCAA 548

>emb|X13710.1|HSPEROXP  H.sapiens unspliced mRNA for glutathione peroxidase
 Length=1100

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
 (Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
Sbjct 219 CTCGGCTTCCCGTGCAA 235

>emb|X13709.1|HSPEROXR  Human gpox1 mRNA for glutathione peroxidase
Length=819

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
Sbjct 219 CTCGGCTTCCCGTGCAA 235

>ref|NM_001085444.1|  Oryctolagus cuniculus glutathione peroxidase 1 (GPX1),
emb|X13837.1|OCGPO  Rabbit mRNA for glutathione peroxidase (EC 1.11.1.9)
Length=760

GENE ID: 100009258 GPX1 | glutathione peroxidase 1 [Oryctolagus cuniculus]
(10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
Sbjct 229 CTCGGCTTCCCGTGCAA 245

>gb|M21304.1|HUMGLP  Human glutathione peroxidase (GPX1) mRNA, complete cds
Length=856

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
Sbjct 255 CTCGGCTTCCCGTGCAA 271

>gb|U39842.1|CPU39842 Cavia porcellus glutathione peroxidase mRNA, partial cds
Length=331

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
Sbjct 112 CTCGGCTTCCCGTGCAA 128

>emb|CR626479.1|  full-length cDNA clone CS0CAP001YI17 of Thymus of Homo sapi
(human)
Length=838

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)

Strand=Plus/Plus

Query	1	CTCGGCTTCCCGTGCAA	17
Sbjct	234	CTCGGCTTCCCGTGCAA	250

>emb|CR620255.1|  full-length cDNA clone CS0DD004YA07 of Neuroblastoma Cot 50 of Homo sapiens (human)
Length=828

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query	1	CTCGGCTTCCC GTGCAA	17
Sbjct	243	CTCGGCTTCCC GTGCAA	259

>emb|CR614747.1|  full-length cDNA clone CS0DI086YP09 of Placenta Cot 25-normal of Homo sapiens (human)
Length=849

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query	1	CTCGGCTTCCCCTGCAA	17
Subj	268	CTCGGCTTCCCCTGCAA	284

>emb|CR601795.1|  full-length cDNA clone CS0DI068YJ17 of Placenta Cot 25-normal of *Homo sapiens* (human)
Length=792

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query	1	CTCGGCTTCCCCTGCAA	17
Sbjct	188	CTCGGCTTCCCCTGCAA	204

>emb|CR595371.1|  full-length cDNA clone CS0DC025YE23 of Neuroblastoma Cot 25 of Homo sapiens (human)
Length=849

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query	1	CTCGGCTTCCCCTGCAA	17
Sbjct	245	CTCGGCTTCCCCTGCAA	261

>dbEST|AK130160_1| Homo sapiens cDNA FLJ26650 fis. clone MPE04848, highly simi

to Glutathione peroxidase (EC 1.11.1.9)
Length=863

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 261 CTCGGCTTCCCGTGCAA 277

>gb|AC121247.2|  Homo sapiens chromosome 3 clone RP11-3B7, complete sequence
Length=170787

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 22842 CTCGGCTTCCCGTGCAA 22858

>dbj|AB105162.1| Macaca fuscata mRNA for cytosolic glutathione peroxidase, compl
cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 214 CTCGGCTTCCCGTGCAA 230

>ref|NM_000581.2|  Homo sapiens glutathione peroxidase 1 (GPX1), transcript
1, mRNA
Length=921

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 300 CTCGGCTTCCCGTGCAA 316

>ref|NM_201397.1|  Homo sapiens glutathione peroxidase 1 (GPX1), transcript
2, mRNA
Length=1200

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||||||||||||||||
Sbjct 300 CTCGGCTTCCCGTGCAA 316

>gb|CP001111.1|  Stenotrophomonas maltophilia R551-3, complete genome